

SEQUENCE LISTING

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 Bohlmann, Joerg
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<120> MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)

<130> WSUR18414

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<150> 09/360,545

<151> 1999-07-26

<150> 60/052,249

<151> 1997-07-11

<150> PCT/US98/14528

<151> 1998-07-10

<160> 107

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Abies grandis

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<222> (69)..(1952)

<223> Clone AG2.2 encoding myrcene synthase

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 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
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ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
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aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
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cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
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caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
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ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350

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80						85					90					
gct	gag	aga	tta	att	gtg	gag	gta	aag	aag	ata	ttc	aat	tca	atg	tac	398
Ala	Glu	Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	
95					100					105					110	
ctg	gat	gat	gga	aga	tta	atg	agt	tcc	ttt	aat	gat	ctc	atg	caa	cgc	446
Leu	Asp	Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	
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Leu	Trp	Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	
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Lys	Asn	Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	
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175					180					185					190	
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Ser	Pro	Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	
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Cys	Ser	Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	
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tat	cgg	gct	tcc	ctc	att	gcc	ttc	cct	ggt	gag	aaa	gtt	atg	gaa	gaa	782
Tyr	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	
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Ala	Glu	Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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Pro	Val	Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	
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Trp	His	Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	
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Gln	Lys	Glu	Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	

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gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly 355 360 365			1166
ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp 370 375 380			1214
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aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys 400 405 410			1310
gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala 415 420 425 430			1358
gag aag act caa ggg aga aac act ctc aac tat gtt cga aag gct tgg Glu Lys Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp 435 440 445			1406
gag gct tat ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat Glu Ala Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn 450 455 460			1454
ggg tat ctg cca atg ttt gaa gag tac cat gag aat ggg aaa gtg agc Gly Tyr Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser 465 470 475			1502
tct gca tat cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca Ser Ala Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala 480 485 490			1550
tgg ctt cct gat tac atc ttg aag gga att gat ttt cca tcc agg ttc Trp Leu Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe 495 500 505 510			1598
aat gat ttg gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys 515 520 525			1646
tac aag gcc gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys 530 535 540			1694
tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His 545 550 555			1742
atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu 560 565 570			1790

1118 1166 1214 1262 1310 1358 1406 1454 1502 1550 1598 1646 1694 1742 1790

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 Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe
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 Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe
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 Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
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 Glu Ser Met Leu Phe
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Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
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Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
 65 70 75 80

Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
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Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
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Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
 115 120 125

Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
 130 135 140

Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
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Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
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Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
180 185 190

Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
195 200 205

Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
210 215 220

Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
225 230 235 240

Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
245 250 255

Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
260 265 270

Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
275 280 285

Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
290 295 300

Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys
305 310 315 320

Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
325 330 335

Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
340 345 350

Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
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Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
370 375 380

Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
385 390 395 400

Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
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Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
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Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
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Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
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Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
485 490 495

Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
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Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
515 520 525

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Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
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Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
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Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
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Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
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His Lys Ser Leu Ile Ser Ser Thr His Glu Leu Lys Ala Leu Ser Arg
20 25 30

aca att cca gct cta gga atg agt agg cga ggg aaa tct atc act cct 146
Thr Ile Pro Ala Leu Gly Met Ser Arg Arg Gly Lys Ser Ile Thr Pro
35 40 45

tcc atc agc atg agc tct acc acc gtt gta acc gat gat ggt gta cga 194
Ser Ile Ser Met Ser Ser Thr Thr Val Val Thr Asp Asp Gly Val Arg
50 55 60

aga cgc atg ggc gat ttc cat tcc aac ctc tgg gac gat gat gtc ata 242
Arg Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile
65 70 75

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Gln	Ser	Leu	Pro	Thr	Ala	Tyr	Glu	Glu	Lys	Ser	Tyr	Leu	Glu	Arg	Ala	
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Glu	Lys	Leu	Ile	Gly	Glu	Val	Lys	Asn	Met	Phe	Asn	Ser	Met	Ser	Leu	
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gaa	gat	gga	gag	tta	atg	agt	ccg	ctc	aat	gat	ctc	att	caa	cgc	ctt	386
Glu	Asp	Gly	Glu	Leu	Met	Ser	Pro	Leu	Asn	Asp	Leu	Ile	Gln	Arg	Leu	
			115					120					125			
tgg	att	gtc	gac	agc	ctt	gaa	cgt	ttg	ggg	atc	cat	aga	cat	ttc	aaa	434
Trp	Ile	Val	Asp	Ser	Leu	Glu	Arg	Leu	Gly	Ile	His	Arg	His	Phe	Lys	
		130					135					140				
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Asp	Glu	Ile	Lys	Ser	Ala	Leu	Asp	Tyr	Val	Tyr	Ser	Tyr	Trp	Gly	Glu	
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Asn	Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser	Val	Val	Thr	Asp	Leu	Asn	Ser	
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Thr	Ala	Leu	Gly	Leu	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Pro	Val	Ser	
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Ser	Asp	Val	Phe	Lys	Ala	Phe	Lys	Gly	Gln	Asn	Gly	Gln	Phe	Ser	Cys	
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Ser	Glu	Asn	Ile	Gln	Thr	Asp	Glu	Glu	Ile	Arg	Gly	Val	Leu	Asn	Leu	
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Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Ile	Met	Asp	Glu	
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Ala	Glu	Ile	Phe	Ser	Thr	Lys	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	
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Pro	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Gly	Asp	Val	Leu	Glu	Tyr	Gly	
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Trp	His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	
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Lys Arg Glu Leu Glu Ser Leu Val Arg Trp Trp Lys Glu Ser Gly Phe	
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Pro Glu Met Thr Phe Cys Arg His Arg His Val Glu Tyr Tyr Thr Leu	
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Ala Ser Cys Ile Ala Phe Glu Pro Gln His Ser Gly Phe Arg Leu Gly	
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Phe Ala Lys Thr Cys His Leu Ile Thr Val Leu Asp Asp Met Tyr Asp	
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Thr Phe Gly Thr Val Asp Glu Leu Glu Leu Phe Thr Ala Thr Met Lys	
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Arg Trp Asp Pro Ser Ser Ile Asp Cys Leu Pro Glu Tyr Met Lys Gly	
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Val Tyr Ile Ala Val Tyr Asp Thr Val Asn Glu Met Ala Arg Glu Ala	
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Glu Glu Ala Gln Gly Arg Asp Thr Leu Thr Tyr Ala Arg Glu Ala Trp	
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Glu Ala Tyr Ile Asp Ser Tyr Met Gln Glu Ala Arg Trp Ile Ala Thr	
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Gly Tyr Leu Pro Ser Phe Asp Glu Tyr Tyr Glu Asn Gly Lys Val Ser	
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Cys Gly His Arg Ile Ser Ala Leu Gln Pro Ile Leu Thr Met Asp Ile	
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Pro Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu	
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Asn Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys	
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Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys	
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Tyr Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His	
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Ile Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu
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Leu Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe
580 585 590

gac atc gcc aga gct ttc cat tac ggc tac aaa tac cga gac ggc tac 1826
Asp Ile Ala Arg Ala Phe His Tyr Gly Tyr Lys Tyr Arg Asp Gly Tyr
595 600 605

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Ser Val Ala Asn Val Glu Thr Lys Ser Leu Val Thr Arg Thr Leu Leu
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gaa tct gtg cct ttg tag caacagctca aatctatgcc ctatgctatg 1922
Glu Ser Val Pro Leu
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Arg Met Gly Asp Phe His Ser Asn Leu Trp Asp Asp Asp Val Ile Gln
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Ser Leu Pro Thr Ala Tyr Glu Glu Lys Ser Tyr Leu Glu Arg Ala Glu
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Lys Leu Ile Gly Glu Val Lys Asn Met Phe Asn Ser Met Ser Leu Glu
100 105 110

Asp Gly Glu Leu Met Ser Pro Leu Asn Asp Leu Ile Gln Arg Leu Trp
115 120 125

Ile Val Asp Ser Leu Glu Arg Leu Gly Ile His Arg His Phe Lys Asp
130 135 140

Glu Ile Lys Ser Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Gly Glu Asn
145 150 155 160

Gly Ile Gly Cys Gly Arg Glu Ser Val Val Thr Asp Leu Asn Ser Thr

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Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Ile	Met	Asp	Glu	Ala
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His	Thr	Tyr	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Gln	Val	Phe
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Glu	Met	Thr	Phe	Cys	Arg	His	Arg	His	Val	Glu	Tyr	Tyr	Thr	Leu	Ala
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Ala	Lys	Thr	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Met	Tyr	Asp	Thr
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Phe	Gly	Thr	Val	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Thr	Met	Lys	Arg
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Trp	Asp	Pro	Ser	Ser	Ile	Asp	Cys	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val
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Glu	Ala	Gln	Gly	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Arg	Glu	Ala	Trp	Glu
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Ala	Tyr	Ile	Asp	Ser	Tyr	Met	Gln	Glu	Ala	Arg	Trp	Ile	Ala	Thr	Gly
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Tyr	Leu	Pro	Ser	Phe	Asp	Glu	Tyr	Tyr	Glu	Asn	Gly	Lys	Val	Ser	Cys
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Gly	His	Arg	Ile	Ser	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp	Ile	Pro
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450 455 460
465 470 475 480
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Asp Leu Ala Cys Ala Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
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Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ser Ile Ser Cys Tyr
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Met Lys Asp Asn Pro Gly Val Ser Glu Glu Asp Ala Leu Asp His Ile
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Asn Ala Met Ile Ser Asp Val Ile Lys Gly Leu Asn Trp Glu Leu Leu
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Lys Pro Asp Ile Asn Val Pro Ile Ser Ala Lys Lys His Ala Phe Asp
580 585 590

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Leu Cys Ile Ser Thr Ala Val Pro Thr Leu Arg Met Arg Arg Arg Gln
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Asp Asn Gly Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro
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Gly Ser Ser Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys	
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Glu Met Phe Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln	
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Asn Asp Leu Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu	
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Gly Ile Asp Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr	
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Val Tyr Ser Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp	
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Ser Thr Phe Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu	
175 180 185	
cga ctg cac gga tac aat gtg tct tca gat gtg ctg gaa tac ttc aaa	687
Arg Leu His Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys	
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Asp Glu Lys Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln	
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Ile Thr Arg Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe	
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Leu Lys Lys Val Leu Gln Lys Ile Pro Val Ser Asn Leu Ser Gly Glu	
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Lys Leu Glu Phe Asn Ile Phe His Ser Leu Gln Leu Arg Glu Leu Gln	
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Ser Ile Ser Arg Trp Trp Lys Glu Ser Gly Ser Ser Gln Leu Thr Phe	
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Thr Arg His Arg His Val Glu Tyr Tyr Thr Met Ala Ser Cys Ile Ser	
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Met Leu Pro Lys His Ser Ala Phe Arg Met Glu Phe Val Lys Val Cys	
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His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe Gly Thr Met	
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Thr Thr Arg Trp Leu Pro Glu Tyr Met Lys Gly Val Tyr Met Asp Leu	
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Tyr Gln Cys Ile Asn Glu Met Val Glu Glu Ala Glu Lys Thr Gln Gly	
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Arg Asp Met Leu Asn Tyr Ile Gln Asn Ala Trp Glu Ala Leu Phe Asp	
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Thr Phe Met Gln Glu Ala Lys Trp Ile Ser Ser Ser Tyr Leu Pro Thr	
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480 485 490	
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Ala Thr Leu Gln Pro Ile Leu Thr Leu Asp Val Pro Leu Pro Asp Tyr	
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Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg Phe Asn Glu Leu Ala Ser	
510 515 520 525	
tcc atc ctt cga cta cga ggt gac acg cgc tgc tac aag gcg gat agg	1695
Ser Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg	
530 535 540	
gcc cgt gga gaa gaa gct tca gct ata tgc tgt tat atg aaa gac cat	1743
Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser Cys Tyr Met Lys Asp His	
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Pro Gly Ser Ile Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile
560 565 570

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575 580 585

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590 595 600 605

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625 630 635

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Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
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Gly Gly Val Leu Gln Arg Arg Ile Ala Asp His His Pro Asn Leu Trp
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Glu Asp Asp Phe Ile Gln Ser Leu Ser Ser Pro Tyr Gly Gly Ser Ser
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Tyr Ser Glu Arg Ala Glu Thr Val Val Glu Glu Val Lys Glu Met Phe
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Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
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130 135 140

Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
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Pro	Asp	Leu	Asn	Ser	Thr	Ala	Leu	Ala	Leu	Arg	Thr	Leu	Arg	Leu	His		
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Lys	His	Ser	Ala	Phe	Arg	Met	Glu	Phe	Val	Lys	Val	Cys	His	Leu	Val		
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Thr	Val	Leu	Asp	Asp	Ile	Tyr	Asp	Thr	Phe	Gly	Thr	Met	Asn	Glu	Leu		
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Gln	Leu	Phe	Thr	Asp	Ala	Ile	Lys	Arg	Trp	Asp	Leu	Ser	Thr	Thr	Arg		
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Trp	Leu	Pro	Glu	Tyr	Met	Lys	Gly	Val	Tyr	Met	Asp	Leu	Tyr	Gln	Cys		
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Ile	Asn	Glu	Met	Val	Glu	Glu	Ala	Glu	Lys	Thr	Gln	Gly	Arg	Asp	Met		
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Leu	Asn	Tyr	Ile	Gln	Asn	Ala	Trp	Glu	Ala	Leu	Phe	Asp	Thr	Phe	Met		
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Gln	Glu	Ala	Lys	Trp	Ile	Ser	Ser	Ser	Tyr	Leu	Pro	Thr	Phe	Glu	Glu		
465					470					475					480		
Tyr	Leu	Lys	Asn	Ala	Lys	Val	Ser	Ser	Gly	Ser	Arg	Ile	Ala	Thr	Leu		

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485										490					495				
Gln	Pro	Ile	Leu	Thr	Leu	Asp	Val	Pro	Leu	Pro	Asp	Tyr	Ile	Leu	Gln				
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Glu	Ile	Asp	Tyr	Pro	Ser	Arg	Phe	Asn	Glu	Leu	Ala	Ser	Ser	Ile	Leu				
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Arg	Leu	Arg	Gly	Asp	Thr	Arg	Cys	Tyr	Lys	Ala	Asp	Arg	Ala	Arg	Gly				
		530				535					540								
Glu	Glu	Ala	Ser	Ala	Ile	Ser	Cys	Tyr	Met	Lys	Asp	His	Pro	Gly	Ser				
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Ile	Glu	Glu	Asp	Ala	Leu	Asn	His	Ile	Asn	Ala	Met	Ile	Ser	Asp	Ala				
				565				570						575					
Ile	Arg	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Pro	Asp	Ser	Lys	Ser	Pro				
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Ile	Ser	Ser	Lys	Lys	His	Ala	Phe	Asp	Ile	Thr	Arg	Ala	Phe	His	His				
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Val	Tyr	Lys	Tyr	Arg	Asp	Gly	Tyr	Thr	Val	Ser	Asn	Asn	Glu	Thr	Lys				
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<220>

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Tyr Arg Glu Arg Ala Glu Val Leu Val Ser Glu Ile Lys Val Met Leu
20 25 30

aat Asn	cca Pro	gct Ala 35	att Ile	aca Thr	gga Gly	gat Asp	gga Gly 40	gaa Glu	tca Ser	atg Met	att Ile 45	act Thr	cca Pro	tct Ser	gct Ala	145
tat Tyr	gac Asp 50	aca Thr	gca Ala	tgg Trp	gta Val	gcg Ala 55	agg Arg	gtg Val	ccc Pro	gcc Ala	att Ile 60	gat Asp	ggc Gly	tct Ser	gct Ala	193
cgc Arg 65	ccg Pro	caa Gln	ttt Phe	ccc Pro	caa Gln 70	aca Thr	gtt Val	gac Asp	tgg Trp	att Ile 75	ttg Leu	aaa Lys	aac Asn	cag Gln	tta Leu 80	241
aaa Lys	gat Asp	ggt Gly	tca Ser	tgg Trp 85	gga Gly	att Ile	cag Gln	tcc Ser	cac His 90	ttt Phe	ctg Leu	ctg Leu	tcc Ser	gac Asp 95	cgt Arg	289
ctt Leu	ctt Leu	gcc Ala 100	act Thr	ctt Leu	tct Ser	tgt Cys	gtt Val	ctt Leu 105	gtg Val	ctc Leu	ctt Leu	aaa Lys	tgg Trp 110	aac Asn	gtt Val	337
ggg Gly	gat Asp	ctg Leu 115	caa Gln	gta Val	gag Glu	cag Gln	gga Gly 120	att Ile	gaa Glu	ttc Phe	ata Ile 125	aag Lys	agc Ser	aat Asn	ctg Leu	385
gaa Glu	cta Leu 130	gta Val	aag Lys	gat Asp	gaa Glu	acc Thr 135	gat Asp	caa Gln	gat Asp	agc Ser	ttg Leu 140	gta Val	aca Thr	gac Asp	ttt Phe	433
gag Glu 145	atc Ile	ata Ile	ttt Phe	cct Pro	tct Ser 150	ctg Leu	tta Leu	aga Arg	gaa Glu 155	gct Ala	caa Gln	tct Ser	ctg Leu	cgc Arg	ctc Leu 160	481
gga Gly	ctt Leu	ccc Pro	tac Tyr	gac Asp 165	ctg Leu	cct Pro	tat Tyr	ata Ile	cat His 170	ctg Leu	ttg Leu	cag Gln	act Thr	aaa Lys 175	cgg Arg	529
cag Gln	gaa Glu	aga Arg 180	tta Leu	gca Ala	aaa Lys	ctt Leu	tca Ser	agg Arg 185	gag Glu	gaa Glu	att Ile	tat Tyr	gcg Ala 190	gtt Val	ccg Pro	577
tcg Ser	cca Pro	ttg Leu 195	ttg Leu	tat Tyr	tct Ser	tta Leu 200	gag Glu	gga Gly	ata Ile	caa Gln	gat Asp 205	ata Ile	gtt Val	gaa Glu	tgg Trp	625
gaa Glu	cga Arg 210	ata Ile	atg Met	gaa Glu	gtt Val	caa Gln 215	agt Ser	cag Gln	gat Asp	ggg Gly 220	tct Ser 220	ttc Phe	tta Leu	agc Ser	tca Ser	673
cct Pro 225	gct Ala	tct Ser	act Thr	gcc Ala	tgc Cys 230	gtt Val	ttc Phe	atg Met	cac His	aca Thr 235	gga Gly	gac Asp	gcg Ala	aaa Lys	tgc Cys 240	721
ctt Leu	gaa Glu	ttc Phe	ttg Leu	aac Asn 245	agt Ser	gtg Val	atg Met	atc Ile	aag Lys 250	ttt Phe	gga Gly	aat Asn	ttt Phe 255	gtt Val	ccc Pro	769
tgc Cys	ctg Leu	tat Tyr	cct Pro 260	gtg Val	gat Asp	ctg Leu	ctg Leu	gaa Glu 265	cgc Arg	ctg Leu	ttg Leu	atc Ile	gta Val 270	gat Asp	aat Asn	817
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Ile	Val	Arg	Leu	Gly	Ile	Tyr	Arg	His	Phe	Glu	Lys	Glu	Ile	Lys	Glu		
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Ala	Leu	Asp	Tyr	Val	Tyr	Arg	His	Trp	Asn	Glu	Arg	Gly	Ile	Gly	Trp		
	290					295				300							
ggc	aga	cta	aat	ccc	ata	gca	gat	ctt	gag	acc	act	gct	ttg	gga	ttt	961	
Gly	Arg	Leu	Asn	Pro	Ile	Ala	Asp	Leu	Glu	Thr	Thr	Ala	Leu	Gly	Phe		
305					310					315					320		
cga	ttg	ctt	cgg	ctg	cat	agg	tac	aat	gta	tct	cca	gcc	att	ttt	gac	1009	
Arg	Leu	Leu	Arg	Leu	His	Arg	Tyr	Asn	Val	Ser	Pro	Ala	Ile	Phe	Asp		
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aac	ttc	aaa	gat	gcc	aat	ggg	aaa	ttc	att	tgc	tcg	acc	ggt	caa	ttc	1057	
Asn	Phe	Lys	Asp	Ala	Asn	Gly	Lys	Phe	Ile	Cys	Ser	Thr	Gly	Gln	Phe		
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aac	aaa	gat	gta	gca	agc	atg	ctg	aat	ctt	tat	aga	gct	tcc	cag	ctc	1105	
Asn	Lys	Asp	Val	Ala	Ser	Met	Leu	Asn	Leu	Tyr	Arg	Ala	Ser	Gln	Leu		
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Ala	Phe	Pro	Gly	Glu	Asn	Ile	Leu	Asp	Glu	Ala	Lys	Ser	Phe	Ala	Thr		
	370					375					380						
aaa	tat	ttg	aga	gaa	gct	ctt	gag	aaa	agt	gag	act	tcc	agt	gca	tgg	1201	
Lys	Tyr	Leu	Arg	Glu	Ala	Leu	Glu	Lys	Ser	Glu	Thr	Ser	Ser	Ala	Trp		
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Asn	Asn	Lys	Gln	Asn	Leu	Ser	Gln	Glu	Ile	Lys	Tyr	Ala	Leu	Lys	Thr		
				405					410					415			
tct	tgg	cat	gcc	agt	gtt	ccg	aga	gtg	gaa	gca	aag	aga	tac	tgt	caa	1297	
Ser	Trp	His	Ala	Ser	Val	Pro	Arg	Val	Glu	Ala	Lys	Arg	Tyr	Cys	Gln		
			420					425					430				
gtg	tat	cgc	cca	gat	tat	gca	cgc	ata	gca	aaa	tgc	gtt	tac	aag	cta	1345	
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ccg	ctg	gaa	ttc	tac	ttc	tta	gta	gcg	gcg	ggg	acc	tat	gaa	ccc	cag	1537	
Pro	Leu	Glu	Phe	Tyr	Phe	Leu	Val	Ala	Ala	Gly	Thr	Tyr	Glu	Pro	Gln		
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tat	gcc	aaa	tgc	agg	ttc	ctc	ttt	aca	aaa	gtg	gca	tgc	ttg	cag	act	1585	
Tyr	Ala	Lys	Cys	Arg	Phe	Leu	Phe	Thr	Lys	Val	Ala	Cys	Leu	Gln	Thr		

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515						520						525						
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Leu	Phe	Thr	Glu	Ala	Val	Arg	Arg	Trp	Asp	Leu	Ser	Phe	Thr	Glu	Asn			
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ctt	cca	gac	tat	atg	aaa	cta	tgt	tac	caa	atc	tat	tat	gac	ata	gtt	1729		
Leu	Pro	Asp	Tyr	Met	Lys	Leu	Cys	Tyr	Gln	Ile	Tyr	Tyr	Asp	Ile	Val			
565						570						575						
cac	gag	gtg	gct	tgg	gag	gca	gag	aag	gaa	cag	ggg	cgt	gaa	ttg	gtc	1777		
His	Glu	Val	Ala	Trp	Glu	Ala	Glu	Lys	Glu	Gln	Gly	Arg	Glu	Leu	Val			
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agc	ttt	ttc	aga	aag	gga	tgg	gag	gat	tat	ctt	ctg	ggt	tat	tat	gaa	1825		
Ser	Phe	Phe	Arg	Lys	Gly	Trp	Glu	Asp	Tyr	Leu	Leu	Gly	Tyr	Tyr	Glu			
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675						680						685						
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Arg	Gly	Glu	Leu	Ala	Ser	Ser	Ile	Glu	Cys	Tyr	Met	Lys	Asp	His	Pro			
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Pro	Ala	Val	Lys	Glu	Leu	Thr	Arg	Glu	Phe	Leu	Lys	Pro	Asp	Asp	Val			
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gtg	ata	ttc	aag	gat	gga	gat	gga	ttc	ggt	gtt	tcc	aaa	tta	gaa	gtc	2305		
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755						760						765						

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aaa gat cat atc aaa gag tgt ctc att gaa ccg ctg cca ctg taa 2350
 Lys Asp His Ile Lys Glu Cys Leu Ile Glu Pro Leu Pro Leu
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Tyr Asp Thr Ala Trp Val Ala Arg Val Pro Ala Ile Asp Gly Ser Ala
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Arg Pro Gln Phe Pro Gln Thr Val Asp Trp Ile Leu Lys Asn Gln Leu
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Lys Asp Gly Ser Trp Gly Ile Gln Ser His Phe Leu Leu Ser Asp Arg
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Leu Leu Ala Thr Leu Ser Cys Val Leu Val Leu Leu Lys Trp Asn Val
 100 105 110

Gly Asp Leu Gln Val Glu Gln Gly Ile Glu Phe Ile Lys Ser Asn Leu
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Glu Leu Val Lys Asp Glu Thr Asp Gln Asp Ser Leu Val Thr Asp Phe
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Glu Ile Ile Phe Pro Ser Leu Leu Arg Glu Ala Gln Ser Leu Arg Leu
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Gly Leu Pro Tyr Asp Leu Pro Tyr Ile His Leu Leu Gln Thr Lys Arg
 165 170 175

Gln Glu Arg Leu Ala Lys Leu Ser Arg Glu Glu Ile Tyr Ala Val Pro
 180 185 190

Ser Pro Leu Leu Tyr Ser Leu Glu Gly Ile Gln Asp Ile Val Glu Trp
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Glu Arg Ile Met Glu Val Gln Ser Gln Asp Gly Ser Phe Leu Ser Ser
 210 215 220

Pro Ala Ser Thr Ala Cys Val Phe Met His Thr Gly Asp Ala Lys Cys
 225 230 235 240

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 Lys Tyr Leu Arg Glu Ala Leu Glu Lys Ser Glu Thr Ser Ser Ala Trp
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 Ser Trp His Ala Ser Val Pro Arg Val Glu Ala Lys Arg Tyr Cys Gln
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 Val Tyr Arg Pro Asp Tyr Ala Arg Ile Ala Lys Cys Val Tyr Lys Leu
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Pro	Ala	Val	Lys	Glu	Leu	Thr	Arg	Glu	Phe	Leu	Lys	Pro	Asp	Asp	Val															
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Pro	Phe	Ala	Cys	Lys	Lys	Met	Leu	Phe	Glu	Glu	Thr	Arg	Val	Thr	Met															
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gtg	tgg	gac	gat	gac	ctc	ata	cac	tct	ctc	aac	tcg	ccc	tat	ggg	gca	95				
Val	Trp	Asp	Asp	Asp	Leu	Ile	His	Ser	Leu	Asn	Ser	Pro	Tyr	Gly	Ala					
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Pro	Ala	Tyr	Tyr	Glu	Leu	Leu	Gln	Lys	Leu	Ile	Glu	Glu	Ile	Lys	His	
			35				40						45			
tta	ctt	ttg	act	gaa	atg	gaa	atg	gat	gat	ggc	gat	cat	gat	tta	atc	191
Leu	Leu	Leu	Thr	Glu	Met	Glu	Met	Asp	Asp	Gly	Asp	His	Asp	Leu	Ile	
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aaa	cgt	ctt	cag	atc	gtt	gac	act	ttg	gaa	tgc	ctg	gga	atc	gat	aga	239
Lys	Arg	Leu	Gln	Ile	Val	Asp	Thr	Leu	Glu	Cys	Leu	Gly	Ile	Asp	Arg	
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cat	ttt	gaa	cac	gaa	ata	caa	aca	gct	gct	tta	gat	tac	gtt	tac	aga	287
His	Phe	Glu	His	Glu	Ile	Gln	Thr	Ala	Ala	Leu	Asp	Tyr	Val	Tyr	Arg	
			80				85						90			
tg	tg	aac	gaa	aaa	ggt	atc	ggg	gag	gga	tca	aga	gat	tcc	ttc	agc	335
Trp	Trp	Asn	Glu	Lys	Gly	Ile	Gly	Glu	Gly	Ser	Arg	Asp	Ser	Phe	Ser	
			100				105						110			
aaa	gat	ctc	aac	gct	aca	gct	tta	gga	ttt	cgc	gct	ctc	cga	ctg	cat	383
Lys	Asp	Leu	Asn	Ala	Thr	Ala	Leu	Gly	Phe	Arg	Ala	Leu	Arg	Leu	His	
			115				120						125			
cga	tat	aac	gta	tcg	tca	ggt	gtg	ttg	aag	aat	ttc	aag	gat	gaa	aac	431
Arg	Tyr	Asn	Val	Ser	Ser	Gly	Val	Leu	Lys	Asn	Phe	Lys	Asp	Glu	Asn	
			130				135						140			
ggg	aag	ttc	ttc	tgc	aac	ttt	act	ggt	gaa	gaa	gga	aga	gga	gat	aaa	479
Gly	Lys	Phe	Phe	Cys	Asn	Phe	Thr	Gly	Glu	Glu	Gly	Arg	Gly	Asp	Lys	
			145				150						155			
caa	gtg	aga	agc	atg	ttg	tcg	tta	ctt	cga	gct	tca	gag	att	tcg	ttt	527
Gln	Val	Arg	Ser	Met	Leu	Ser	Leu	Leu	Arg	Ala	Ser	Glu	Ile	Ser	Phe	
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ccc	gga	gaa	aaa	gtg	atg	gaa	gag	gcc	aag	gca	ttc	aca	aga	gaa	tat	575
Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Arg	Glu	Tyr	
			180				185						190			
cta	aac	caa	gtt	tta	gct	gga	cac	ggg	gat	gtg	act	gac	gtg	gat	caa	623
Leu	Asn	Gln	Val	Leu	Ala	Gly	His	Gly	Asp	Val	Thr	Asp	Val	Asp	Gln	
			195				200						205			
agc	ctt	ttg	gag	aga	ggt	gaa	gta	cgc	att	gga	gtt	tcc	atg	gct	tgc	671
Ser	Leu	Leu	Glu	Arg	Gly	Glu	Val	Arg	Ile	Gly	Val	Ser	Met	Ala	Cys	
			210				215						220			
agt	gtg	ccg	aga	tg	gag	gca	agg	agc	ttt	ctc	gaa	ata	tat	gga	cac	719
Ser	Val	Pro	Arg	Trp	Glu	Ala	Arg	Ser	Phe	Leu	Glu	Ile	Tyr	Gly	His	
			225				230						235			
aac	cat	tcg	tg	ctc	aag	tcg	aat	atc	aac	caa	aaa	atg	ttg	aag	tta	767
Asn	His	Ser	Trp	Leu	Lys	Ser	Asn	Ile	Asn	Gln	Lys	Met	Leu	Lys	Leu	
			240				245						250			
gcc	aaa	ttg	gac	ttc	aat	att	ctg	caa	tgc	aaa	cat	cac	aag	gag	ata	815
Ala	Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Lys	His	His				

Gln	Phe	Ile	Thr	Arg	Trp	Trp	Arg	Asp	Ser	Gly	Ile	Ser	Gln	Leu	Asn	
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Phe	Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys	
			290				295						300			
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Ile	Phe	Glu	Pro	Glu	Phe	Ser	Glu	Ser	Arg	Ile	Ala	Phe	Ala	Lys	Thr	
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Ala	Ile	Leu	Cys	Thr	Val	Leu	Asp	Asp	Leu	Tyr	Asp	Thr	His	Ala	Thr	
			320				325						330			335
ttg	cat	gaa	atc	aaa	atc	atg	aca	gag	gga	gtg	aga	cga	tgg	gat	ctt	1055
Leu	His	Glu	Ile	Lys	Ile	Met	Thr	Glu	Gly	Val	Arg	Arg	Trp	Asp	Leu	
			340				345						350			
tcg	ttg	aca	gat	gac	ctc	cca	gac	tac	att	aaa	att	gca	ttc	cag	ttc	1103
Ser	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Tyr	Ile	Lys	Ile	Ala	Phe	Gln	Phe	
			355				360						365			
ttc	ttc	aat	aca	gtg	aat	gaa	ttg	ata	gtt	gaa	atc	gtg	aaa	cgg	caa	1151
Phe	Phe	Asn	Thr	Val	Asn	Glu	Leu	Ile	Val	Glu	Ile	Val	Lys	Arg	Gln	
			370				375						380			
ggg	cgg	gat	atg	aca	acc	ata	gtt	aaa	gat	tgc	tgg	aag	cga	tac	att	1199
Gly	Arg	Asp	Met	Thr	Thr	Ile	Val	Lys	Asp	Cys	Trp	Lys	Arg	Tyr	Ile	
			385				390						395			
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Glu	Ser	Tyr	Leu	Gln	Glu	Ala	Glu	Trp	Ile	Ala	Thr	Gly	His	Ile	Pro	
			400				405						410			415
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Thr	Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	
			420				425						430			
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Ile	Val	Asn	Leu	Asn	Pro	Leu	Leu	Leu	Leu	Gly	Lys	Leu	Leu	Pro	Asp	
			435				440						445			
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Asn	Ile	Leu	Glu	Gln	Ile	His	Ser	Pro	Ser	Lys	Ile	Leu	Asp	Leu	Leu	
			450				455						460			
gaa	ttg	acg	ggc	aga	atc	gcc	gat	gac	tta	aaa	gat	ttc	gag	gac	gag	1439
Glu	Leu	Thr	Gly	Arg	Ile	Ala	Asp	Asp	Leu	Lys	Asp	Phe	Glu	Asp	Glu	
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Lys	Glu	Arg	Gly	Glu	Met	Ala	Ser	Ser	Leu	Gln	Cys	Tyr	Met	Lys	Glu	
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Glu Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met				
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Glu Glu				
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Tyr Asn Val Ser Ser Gly Val Leu Lys Asn Phe Lys Asp Glu Asn Gly				
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Lys Phe Phe Cys Asn Phe Thr Gly Glu Glu Gly Arg Gly Asp Lys Gln				
145 150 155 160				

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Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Lys	Ala	Phe	Thr	Arg	Glu	Tyr	Leu	180	185	190
Asn	Gln	Val	Leu	Ala	Gly	His	Gly	Asp	Val	Thr	Asp	Val	Asp	Gln	Ser	195	200	205
Leu	Leu	Glu	Arg	Gly	Glu	Val	Arg	Ile	Gly	Val	Ser	Met	Ala	Cys	Ser	210	215	220
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His	Ser	Trp	Leu	Lys	Ser	Asn	Ile	Asn	Gln	Lys	Met	Leu	Lys	Leu	Ala	245	250	255
Lys	Leu	Asp	Phe	Asn	Ile	Leu	Gln	Cys	Lys	His	His	Lys	Glu	Ile	Gln	260	265	270
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Tyr	Arg	Lys	Arg	His	Val	Glu	Tyr	Tyr	Ser	Trp	Val	Val	Met	Cys	Ile	290	295	300
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Phe	Asn	Glu	Tyr	Ile	Lys	Asn	Gly	Met	Ala	Ser	Ser	Gly	Met	Cys	Ile	420	425	430
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Asn Arg Ser Leu Glu Glu Phe Asn Trp Glu Phe Met Lys Gln Asp Ser
515 520 525

Val Pro Met Cys Cys Lys Lys Phe Thr Phe Asn Ile Gly Arg Gly Leu
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Val Lys Asp Gln Ile Phe Lys Ile Leu Val His Gln Val Pro Met Glu
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Lys Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu
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Gly Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln
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Arg Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser
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gag ctt aag tcg aat ttg agc aaa aaa atg tta gag ttg gcg aaa ttg 239
Glu Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu
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gac ttc aat att ctg caa tgc aca cat cag aaa gaa ctg cag att atc 287
Asp Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile
80 85 90 95

tca agg tgg ttc gca gac tca agt ata gca tcc ctg aat ttc tat cgg 335
Ser Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg
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atg Met	aca Thr 145	atg Met	cta Leu	gat Asp	gac Asp	ctg Leu 150	tac Tyr	gat Asp	act Thr	cac His	gga Gly 155	acc Thr	ttg Leu	gac Asp	caa Gln	479
ctc Leu 160	aaa Lys	atc Ile	ttt Phe	aca Thr	gag Glu 165	gga Gly	gtg Val	aga Arg	cga Arg	tgg Trp 170	gat Asp	gtt Val	tcg Ser	ttg Leu	gta Val 175	527
gag Glu	ggc Gly	ctc Leu	cca Pro	gac Asp 180	ttc Phe	atg Met	aaa Lys	att Ile	gca Ala 185	ttc Phe	gag Glu	ttc Phe	tgg Trp	tta Leu 190	aag Lys	575
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atg Met	gcg Ala 210	gcc Ala	tac Tyr	ata Ile	aga Arg	aaa Lys	aat Asn 215	gca Ala	tgg Trp	gag Glu	cga Arg	tac Tyr 220	ctt Leu	gaa Glu	gct Ala	671
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gat Asp 240	gag Glu	tac Tyr	ttg Leu	aat Asn 245	aat Asn	ggc Gly	aca Thr	cca Pro	aac Asn	act Thr 250	ggg Gly	atg Met	tgt Cys	gta Val	ttg Leu 255	767
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ctg Leu	gag Glu	caa Gln	ata Ile 275	ttc Phe	ttg Leu	ccc Pro	tcc Ser	agg Arg 280	ttc Phe	cac His	cat His	ctc Leu	att Ile 285	gaa Glu	ttg Leu	863
gct Ala	tcc Ser	agg Arg 290	ctc Leu	gtc Val	gat Asp	gac Asp	gcg Ala 295	aga Arg	gat Asp	ttc Phe	cag Gln	gcg Ala 300	gag Glu	aag Lys	gat Asp	911
cat His	ggg Gly 305	gat Asp	tta Leu	tcg Ser	tgt Cys	att Ile 310	gag Glu	tgt Cys	tat Tyr	tta Leu	aaa Lys 315	gat Asp	cat His	cct Pro	gag Glu	959
tct Ser 320	aca Thr	gta Val	gaa Glu	gat Asp	gct Ala 325	tta Leu	aat Asn	cat His	gtt Val	aat Asn 330	ggc Gly	ctc Leu	ctt Leu	ggc Gly	aat Asn 335	1007
tgc Cys	ctt Leu	ctg Leu	gaa Glu	atg Met 340	aat Asn	tgg Trp	aag Lys	ttc Phe	tta Leu 345	aag Lys	aag Lys	cag Gln	gac Asp	agt Ser 350	gtg Val	1055
cca Pro	ctc Leu	tcg Ser	tgt Cys	aag Lys	aag Lys	tac Tyr	agc Ser	ttc Phe	cat His	gta Val	ttg Leu	gca Ala	cga Arg	agc Ser	atc Ile	1103

355	360	365	
caa ttc atg tac aat caa ggc gat ggc ttc tcc att tcg aac aaa gtg			1151
Gln Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val			
370	375	380	
atc aag gat caa gtg cag aaa gtt ctt att gtc ccc gtg cct att tga			1199
Ile Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile			
385	390	395	
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aatgctgatg atggtaaag tccattcaga ccaatctttg gtttattgga cttaaataaa			1319
tgaattaatt agtttgtttt aaaattgtac tatttactgt tggaataat gttttcatta			1379
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Val Leu Ala Gly Arg Glu Ala Thr His Val Asp Glu Ser Leu Leu Gly			
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Glu Val Lys Tyr Ala Leu Glu Phe Pro Trp His Cys Ser Val Gln Arg			
35	40	45	
Trp Glu Ala Arg Ser Phe Ile Glu Ile Phe Gly Gln Ile Asp Ser Glu			
50	55	60	
Leu Lys Ser Asn Leu Ser Lys Lys Met Leu Glu Leu Ala Lys Leu Asp			
65	70	75	80
Phe Asn Ile Leu Gln Cys Thr His Gln Lys Glu Leu Gln Ile Ile Ser			
85	90	95	
Arg Trp Phe Ala Asp Ser Ser Ile Ala Ser Leu Asn Phe Tyr Arg Lys			
100	105	110	
Cys Tyr Val Glu Phe Tyr Phe Trp Met Ala Ala Ala Ile Ser Glu Pro			
115	120	125	
Glu Phe Ser Gly Ser Arg Val Ala Phe Thr Lys Ile Ala Ile Leu Met			
130	135	140	
Thr Met Leu Asp Asp Leu Tyr Asp Thr His Gly Thr Leu Asp Gln Leu			
145	150	155	160
Lys Ile Phe Thr Glu Gly Val Arg Arg Trp Asp Val Ser Leu Val Glu			
165	170	175	
Gly Leu Pro Asp Phe Met Lys Ile Ala Phe Glu Phe Trp Leu Lys Thr			
180	185	190	

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Ser Asn Glu Leu Ile Ala Glu Ala Val Lys Ala Gln Gly Gln Asp Met
195 200 205

Ala Ala Tyr Ile Arg Lys Asn Ala Trp Glu Arg Tyr Leu Glu Ala Tyr
210 215 220

Leu Gln Asp Ala Glu Trp Ile Ala Thr Gly His Val Pro Thr Phe Asp
225 230 235 240

Glu Tyr Leu Asn Asn Gly Thr Pro Asn Thr Gly Met Cys Val Leu Asn
245 250 255

Leu Ile Pro Leu Leu Leu Met Gly Glu His Leu Pro Ile Asp Ile Leu
260 265 270

Glu Gln Ile Phe Leu Pro Ser Arg Phe His His Leu Ile Glu Leu Ala
275 280 285

Ser Arg Leu Val Asp Asp Ala Arg Asp Phe Gln Ala Glu Lys Asp His
290 295 300

Gly Asp Leu Ser Cys Ile Glu Cys Tyr Leu Lys Asp His Pro Glu Ser
305 310 315 320

Thr Val Glu Asp Ala Leu Asn His Val Asn Gly Leu Leu Gly Asn Cys
325 330 335

Leu Leu Glu Met Asn Trp Lys Phe Leu Lys Lys Gln Asp Ser Val Pro
340 345 350

Leu Ser Cys Lys Lys Tyr Ser Phe His Val Leu Ala Arg Ser Ile Gln
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Phe Met Tyr Asn Gln Gly Asp Gly Phe Ser Ile Ser Asn Lys Val Ile
370 375 380

Lys Asp Gln Val Gln Lys Val Leu Ile Val Pro Val Pro Ile
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<220>
<223> Description of Artificial Sequence:
oligonucleotide PCR primer E wherein the letter
"n" represents an inosine residue

<220>
<221> misc_feature
<222> (1)..(23)
<223> PCR primer E wherein the letter n represents
inosine

<400> 21
ggngaramrr tnatggarga rgc

<210> 22

<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
oligonucleotide primer F wherein the letter "n"
represents an inosine residue

<220>

<221> misc_feature

<222> (1)..(24)

<223> PCR primer F wherein the letter n represents
inosine

<400> 22

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24

<210> 23

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
oligonucleotide PCR primer G wherein the letter
"n" represents an inosine residue

<220>

<221> misc_feature

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<223> PCR primer G wherein the letter n represents
inosine

<400> 23

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21

<210> 24

<211> 533

<212> DNA

<213> Abies grandis

<400> 24

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cacacatatt tgccgcgatt ggaagcaagg aattacatcc aagtctttgg acaggacact 180

gagaacacga agtcatatgt gaagagcaaa aaacttttag aactcgcaaa attggagttc 240

aacatctttc aatccttact cgcatatccg cattgcaacc cattctgaca atggacatcc 300

cctttcctga tcatatcctc aaggaagttg acttcccatc aaagcttaac gacttggcat 360

gtgccatcct tcgattacga ggtgatacgc ggtgctacaa ggcggacagg gctcgtggag 420

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<210> 25
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<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of Primer D
was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa
at
position number 4 represents Ile or Tyr or Phe, Xaa at position number 6
represents Ala or Val and Xaa at position number 8 represents Ala or Gly

<220>
<221> SITE
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primer D was based

<400> 25
Asp Asp Xaa Xaa Asp Xaa Tyr Xaa
1 5

<210> 26
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif on which the sequence of Primer E
was based wherein Xaa at position 3 represents Lys or Thr, Xaa at
position
4 represents Val or Ile, Xaa at position 6 represents Glu or Asp

<220>
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sequence of primer E was based

<400> 26
Gly Glu Xaa Xaa Met Xaa Glu Ala
1 5

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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amino acid sequence on which the sequence of
primer F was based wherein Xaa at position 2 represents Phe or Tyr or
Asp

Xaa at position 3 represents Ile or Leu, Xaa at position 4 represents Thr or Leu
or Arg

<220>
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<400> 27
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<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
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amino acid motif on which the sequence of primer G
was based wherein Xaa at position 6 represents Phe or Leu

<220>
<221> SITE
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<223> conserved amino acid sequence on which the
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<400> 28
Asp Val Ile Lys Gly Xaa Asn Trp
1 5

<210> 29
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<220>
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<400> 29
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<210> 30
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<220>
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 Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg Lys
 5 10 15

tcg ttg atc agt tca att cat gaa cat aag cct ccc tat aga aca atc 155
 Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr Ile
 20 25 30

cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg cct tcc atg 203
 Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr Pro Ser Met
 35 40 45

agc atc agt ttg gcc acc gct gca cct gat gat ggt gta caa aga cgc 251
 Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg Arg
 50 55 60 65

ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc ata cag tct 299
 Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln Ser
 70 75 80

cta tca acg cat tat ggg gaa ccc tct tac cag gaa cgt gct gag aga 347
 Leu Ser Thr His Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu Arg
 85 90 95

tta att gtg gag gta aag aag ata ttc aat tca atg tac ctg gat gat 395
 Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp Asp
 100 105 110

gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc ctt tgg ata 443
 Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp Ile
 115 120 125

gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc aag aac gag 491
 Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn Glu
 130 135 140 145

ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag gaa aac ggc 539
 Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn Gly
 150 155 160

att gga tgt ggg aga gac agt att gtt act gat ctc aac tca act gcg 587
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 165 170 175

ttg ggg ttt cga act ctt cga tta cac ggg tac act gta tct cca gag 635

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 cacatatcat
 atcaaaggga
 gcaaga
 atg
 Met
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 atctcatgaa
 cataggcat
 aagcctccc
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 atc
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 IleSerPro
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 LysSerCys
 LeuArgLys
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 gaacatagg
 cctccc
 tataragaca
 atc
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 SerIleHis
 GluHisLys
 ProProTyr
 ArgThrIle
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 atgcgtagg
 cgaggcgagg
 gggaaa
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 acgccttcc
 atg
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 ProAsnLeuGly
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Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser	Pro		
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Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg	Ala		
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Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu	Ile		
			230						235					240			
ttc	tcc	aca	aga	tat	ttg	aaa	gaa	gct	cta	caa	aag	att	cca	gtc	tcc	827	
Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val	Ser		
			245					250					255				
gct	ctt	tca	caa	gag	ata	aag	ttt	gtt	atg	gaa	tat	ggc	tgg	cac	aca	875	
Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His	Thr		
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aat	ttg	cca	aga	ttg	gaa	gca	aga	aat	tac	ata	gac	aca	ctt	gag	aaa	923	
Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu	Lys		
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Asp	Thr	Ser	Ala	Trp	Leu	Asn	Lys	Asn	Ala	Gly	Lys	Lys	Leu	Leu	Glu		
	290				295					300					305		
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Leu	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	Asn	Ser	Leu	Gln	Gln	Lys	Glu		
			310					315						320			
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Leu	Gln	Tyr	Leu	Leu	Arg	Trp	Trp	Lys	Glu	Ser	Asp	Leu	Pro	Lys	Leu		
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Thr	Phe	Ala	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Thr	Leu	Ala	Ser	Cys		
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Thr	Ile	Asp	Glu	Leu	Glu	Leu	Phe	Thr	Ser	Ala	Ile	Lys	Arg	Trp	Asn		
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Ser	Ser	Glu	Ile	Glu	His	Leu	Pro	Glu	Tyr	Met	Lys	Cys	Val	Tyr	Met		
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Met	Val	Asn	Asp	Ile	Ile	Lys	Glu	Leu	Asn	Trp	Glu	Leu	Leu	Arg	Ser			
565						570						575						
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Arg	Ala	Leu	His	His	Leu	Tyr	Ile	Tyr	Arg	Asp	Gly	Phe	Ser	Val	Ala			
595						600						605						
aac	aag	gaa	aca	aaa	aaa	ttg	gtt	atg	gaa	aca	ctc	ctt	gaa	tct	atg	1931		
Asn	Lys	Glu	Thr	Lys	Lys	Leu	Val	Met	Glu	Thr	Leu	Leu	Glu	Ser	Met			
610						615						620						625
ctt	ttt	taa	cta	taacc	atc	cata	ata	ata	agc	tata	gct	taa	att	at		1983		
Leu	Phe																	
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gatt	aaaaag	ctagag	ctta	ctagg	ttagt	aacat	gggtga	taaa	agttat	aaaat	gtgag					2103		
ttatag	agat	acccat	gttg	aataat	gaat	tacaaa	aaga	gaaat	tttatg	taga	ataaga					2163		
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 <211> 627
 <212> PRT
 <213> Abies grandis

<400> 32

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			20					25					30		
Ile	Pro	Asn	Leu	Gly	Met	Arg	Arg	Arg	Gly	Lys	Ser	Val	Thr	Pro	Ser
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Met	Ser	Ile	Ser	Leu	Ala	Thr	Ala	Ala	Pro	Asp	Asp	Gly	Val	Gln	Arg
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Arg	Ile	Gly	Asp	Tyr	His	Ser	Asn	Ile	Trp	Asp	Asp	Asp	Phe	Ile	Gln
	65				70					75					80
Ser	Leu	Ser	Thr	His	Tyr	Gly	Glu	Pro	Ser	Tyr	Gln	Glu	Arg	Ala	Glu
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Arg	Leu	Ile	Val	Glu	Val	Lys	Lys	Ile	Phe	Asn	Ser	Met	Tyr	Leu	Asp
			100					105					110		
Asp	Gly	Arg	Leu	Met	Ser	Ser	Phe	Asn	Asp	Leu	Met	Gln	Arg	Leu	Trp
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Ile	Val	Asp	Ser	Val	Glu	Arg	Leu	Gly	Ile	Ala	Arg	His	Phe	Lys	Asn
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Glu	Ile	Thr	Ser	Ala	Leu	Asp	Tyr	Val	Phe	Arg	Tyr	Trp	Glu	Glu	Asn
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Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Ile	Val	Thr	Asp	Leu	Asn	Ser	Thr
			165						170					175	
Ala	Leu	Gly	Phe	Arg	Thr	Leu	Arg	Leu	His	Gly	Tyr	Thr	Val	Ser	Pro
			180					185					190		
Glu	Val	Leu	Lys	Ala	Phe	Gln	Asp	Gln	Asn	Gly	Gln	Phe	Val	Cys	Ser
		195					200					205			
Pro	Gly	Gln	Thr	Glu	Gly	Glu	Ile	Arg	Ser	Val	Leu	Asn	Leu	Tyr	Arg
	210					215					220				
Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	Glu	Ala	Glu
	225				230					235					240
Ile	Phe	Ser	Thr	Arg	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Lys	Ile	Pro	Val
			245						250					255	
Ser	Ala	Leu	Ser	Gln	Glu	Ile	Lys	Phe	Val	Met	Glu	Tyr	Gly	Trp	His
		260						265					270		
Thr	Asn	Leu	Pro	Arg	Leu	Glu	Ala	Arg	Asn	Tyr	Ile	Asp	Thr	Leu	Glu
		275					280					285			

Lys 290	Thr	Ser	Ala	Trp	Leu 295	Asn	Lys	Asn	Ala	Gly 300	Lys	Lys	Leu	Leu	
Glu 305	Leu	Ala	Lys	Leu 310	Glu	Phe	Asn	Ile	Phe 315	Asn	Ser	Leu	Gln	Gln 320	
Glu	Leu	Gln	Tyr	Leu 325	Leu	Arg	Trp	Trp	Lys 330	Glu	Ser	Asp	Leu	Pro 335	
Leu	Thr	Phe	Ala 340	Arg	His	Arg	His	Val 345	Glu	Phe	Tyr	Thr	Leu 350	Ala	Ser
Cys	Ile	Ala 355	Ile	Asp	Pro	Lys	His 360	Ser	Ala	Phe	Arg	Leu 365	Gly	Phe	Ala
Lys	Met 370	Cys	His	Leu	Val	Thr 375	Val	Leu	Asp	Asp	Ile 380	Tyr	Asp	Thr	Phe
Gly 385	Thr	Ile	Asp	Glu	Leu 390	Glu	Leu	Phe	Thr	Ser 395	Ala	Ile	Lys	Arg	Trp 400
Asn	Ser	Ser	Glu	Ile 405	Glu	His	Leu	Pro	Glu 410	Tyr	Met	Lys	Cys	Val 415	Tyr
Met	Val	Val	Phe 420	Glu	Thr	Val	Asn	Glu 425	Leu	Thr	Arg	Glu	Ala 430	Glu	Lys
Thr	Gln	Gly 435	Arg	Asn	Thr	Leu	Asn 440	Tyr	Val	Arg	Lys	Ala 445	Trp	Glu	Ala
Tyr	Phe 450	Asp	Ser	Tyr	Met	Glu 455	Glu	Ala	Lys	Trp	Ile 460	Ser	Asn	Gly	Tyr
Leu 465	Pro	Thr	Phe	Glu	Glu 470	Tyr	His	Glu	Asn	Gly 475	Lys	Val	Ser	Ser	Ala 480
Tyr	Arg	Val	Ala	Thr 485	Leu	Gln	Pro	Ile	Leu 490	Thr	Leu	Asn	Ala	Trp 495	Leu
Pro	Asp	Tyr	Ile 500	Leu	Lys	Gly	Ile	Asp 505	Phe	Pro	Ser	Arg	Phe 510	Asn	Asp
Leu	Ala	Ser 515	Ser	Phe	Leu	Arg	Leu 520	Arg	Gly	Asp	Thr	Arg 525	Cys	Tyr	Lys
Ala	Asp 530	Arg	Asp	Arg	Gly	Glu 535	Glu	Ala	Ser	Cys	Ile 540	Ser	Cys	Tyr	Met
Lys 545	Asp	Asn	Pro	Gly	Ser 550	Thr	Glu	Glu	Asp	Ala 555	Leu	Asn	His	Ile	Asn 560
Ala	Met	Val	Asn	Asp 565	Ile	Ile	Lys	Glu	Leu 570	Asn	Trp	Glu	Leu	Leu 575	Arg
Ser	Asn	Asp	Asn 580	Ile	Pro	Met	Leu	Ala 585	Lys	Lys	His	Ala	Phe 590	Asp	Ile
Thr	Arg	Ala 595	Leu	His	His	Leu	Tyr 600	Ile	Tyr	Arg	Asp	Gly 605	Phe	Ser	Val
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610

615

620

Met Leu Phe

625

<210> 33

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 BamHI

<400> 33

caaagggatc cagaatggct ctgg

24

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 2.2 Not I

<400> 34

agtaagcggc cgcttttttaa tcataccac

30

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 EcoRI

<400> 35

ctgcaggaat tcggcacgag c

21

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3.18 SmaI

<400> 36

catagccccg ggcatagatt tgagctg

27

<210> 37

<211> 30

<212> DNA

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 3-11

<400> 42
cgtaatggaa agctctggcg 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide primer 7-1

<400> 43
ccttacacgc ctttggatgg 20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR
oligonucleotide sequence 7-3

<400> 44
tctgttgatc caggatggtc 20

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: conserved
amino acid motif common to all prenyl transferases wherein Xaa at
position
3 and 4 represents any amino acid

<400> 45
Asp Asp Xaa Xaa Asp
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which oligonucleotide primers can be synthesized that hybridize to the monoterpene synthases of the present invention, wherein Xaa at position 4 represents
Leu or Ile or Val

<400> 46

His Ser Asn Xaa Trp Asp Asp Asp
1 5

<210> 47

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotides can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 47

Ala Leu Asp Tyr Val Tyr
1 5

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to the monoterpene synthases of the present invention

<400> 48

Glu Leu Ala Lys Leu Glu Phe
1 5

<210> 49

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid motif from which degenerate oligonucleotide sequences can be constructed that hybridize to monoterpene synthase clones of the present invention

<400> 49

Arg Trp Trp Lys Glu Ser
1 5

<210> 50
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention, wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 50
Xaa Leu Asp Asp Met Tyr Asp
1 5

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to monoterpene synthase
clones of the present invention wherein Xaa at position 1 represents
Val
or Ile or Leu

<400> 51
Xaa Leu Asp Asp Leu Tyr Asp
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
motif from which oligonucleotide sequences can be
constructed that hybridize to the monoterpene
synthase clones of the present invention, wherein Xaa at position 1
represents Val or Ile or Leu

<400> 52
Xaa Leu Asp Asp Ile Tyr Asp
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

motif from which oligonucleotide sequences can be constructed that hybridize to the monoterpene synthase clones of the present invention, wherein Xaa at position 6 represents Asn or His

<400> 53

Cys Tyr Met Lys Asp Xaa Pro
1 5

<210> 54

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet

<400> 54

atgatgatg

9

<210> 55

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide sequence that corresponds to peptide sequence MetMetMet

<400> 55

tactactac

9

<210> 56

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: exemplary oligonucleotide that corresponds to peptide sequence MetMetMet, n is inosine

<400> 56

nacnacnac

9

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligonucleotide corresponding to amino acid sequence set forth in SEQ ID NO:46

<220>
<221> misc_feature
<222> (1)..(24)
<223> Oligonucleotide that corresponds to the conserved
amino acid sequence set forth in SEQ ID NO:46

<400> 57
gtgtcgttgg agaccctgct gctg 24

<210> 58
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:47

<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:47

<400> 58
cgggagctga tgcagatg 18

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:48

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<221> misc_feature
<222> (1)..(21)
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<400> 59
ctcgagcggg tgcagctcaa g 21

<210> 60
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide that corresponds to amino acid
sequence set forth in SEQ ID NO:49

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<220>
<221> misc_feature
<222> (1)..(18)
<223> Oligonucleotide that corresponds to conserved
amino acid sequence set forth in SEQ ID NO:49

<400> 60
gccaccacct tcctctcg 18

<210> 61
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide sequence corresponding to amino
acid sequence set forth in SEQ ID NO:50

<400> 61
gaggagctgc tgtacatgct g 21

<210> 62
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide corresponding to amino acid
sequence set forth in SEQ ID NO:51

<220>
<221> misc_feature
<222> (1)..(21)
<223> Oligonucleotide corresponding to conserved amino
acid sequence set forth in SEQ ID NO:51

<400> 62
gaggagctgc tggagatgct g 21

<210> 63
<211> 293
<212> DNA
<213> Abies grandis

<400> 63
cttaatgaat tggcgcaaga ggctgagaag actcaaggca gagatacgct caactatatt 60
cgcaatgctt atgagtctca ttttgattcg tttatgcacg aagcaaaatg gatctcaagt 120

<400> 64																
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					Met	Ala	Leu	Leu	Ser	Ile						
									1					5		
act	ccg	ctg	gtt	tcc	agg	tcg	tgc	ctc	agt	tct	tct	cat	gag	att	aag	101
Thr	Pro	Leu	Val	Ser	Arg	Ser	Cys	Leu	Ser	Ser	Ser	His	Glu	Ile	Lys	
			10					15						20		
gct	ctc	cgt	aga	aca	atc	cca	act	ctt	gga	atc	tgc	agg	ccg	ggg	aaa	149
Ala	Leu	Arg	Arg	Thr	Ile	Pro	Thr	Leu	Gly	Ile	Cys	Arg	Pro	Gly	Lys	
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Ser	Val	Ala	His	Ser	Ile	Asn	Met	Cys	Leu	Thr	Ser	Val	Ala	Ser	Thr	
	40					45					50					
gat	tct	gta	cag	aga	cgc	gtg	ggc	aac	tat	cat	tcc	aac	ctg	tgg	gac	245
Asp	Ser	Val	Gln	Arg	Arg	Val	Gly	Asn	Tyr	His	Ser	Asn	Leu	Trp	Asp	
	55				60					65					70	
gat	gat	ttc	ata	cag	tct	ctg	atc	tca	acg	cct	tat	gga	gca	cct	gat	293
Asp	Asp	Phe	Ile	Gln	Ser	Leu	Ile	Ser	Thr	Pro	Tyr	Gly	Ala	Pro	Asp	
			75						80					85		
tac	cgg	gaa	cgt	gct	gac	aga	ctt	att	ggg	gaa	gta	aag	gat	ata	atg	341
Tyr	Arg	Glu	Arg	Ala	Asp	Arg	Leu	Ile	Gly	Glu	Val	Lys	Asp	Ile	Met	
			90					95					100			
ttc	aat	ttc	aag	tcg	ctg	gaa	gat	gga	ggc	aat	gat	ctc	ctt	caa	cga	389
Phe	Asn	Phe	Lys	Ser	Leu	Glu	Asp	Gly	Gly	Asn	Asp	Leu	Leu	Gln	Arg	
		105					110					115				
ctt	ttg	ctg	gtc	gat	gac	gtt	gaa	cgt	ttg	gga	atc	gac	agg	cat	ttc	437
Leu	Leu	Leu	Val	Asp	Asp	Val	Glu	Arg	Leu	Gly	Ile	Asp	Arg	His	Phe	
	120					125					130					
aaa	aaa	gag	ata	aaa	acg	gca	ctc	gat	tat	gtt	aac	agt	tat	tgg	aac	485
Lys	Lys	Glu	Ile	Lys	Thr	Ala	Leu	Asp	Tyr	Val	Asn	Ser	Tyr	Trp	Asn	
	135				140					145					150	
gaa	aaa	ggc	att	gga	tgt	ggg	agg	gag	agt	gtt	gtg	act	gac	ctc	aac	533
Glu	Lys	Gly	Ile	Gly	Cys	Gly	Arg	Glu	Ser	Val	Val	Thr	Asp	Leu	Asn	
				155					160					165		

tca Ser	acc Thr	gcc Ala	ttg Leu 170	ggg Gly	ctt Leu	cga Arg	act Thr	ctc Leu 175	cga Arg	cta Leu	cac His	gga Gly	tac Tyr 180	act Thr	gtg Val	581
tct Ser	tca Ser	gat Asp 185	gtt Val	ttg Leu	aac Asn	gtt Val	ttt Phe 190	aaa Lys	gac Asp	aaa Lys	aat Asn	ggg Gly 195	caa Gln	ttt Phe	tcc Ser	629
tcc Ser	act Thr 200	gcc Ala	aat Asn	att Ile	cag Gln	ata Ile 205	gag Glu	gga Gly	gag Glu	att Ile	aga Arg 210	ggc Gly	gtt Val	ctc Leu	aat Asn	677
tta Leu 215	ttc Phe	agg Arg	gcc Ala	tcc Ser	ctc Leu 220	gtc Val	gcc Ala	ttt Phe	ccc Pro	ggc Gly 225	gag Glu	aaa Lys	gtt Val	atg Met	gat Asp 230	725
gaa Glu	gct Ala	gaa Glu	aca Thr	ttc Phe 235	tct Ser	aca Thr	aaa Lys	tat Tyr	tta Leu 240	aga Arg	gaa Glu	gcc Ala	ctg Leu	caa Gln 245	aag Lys	773
att Ile	ccg Pro	gca Ala	tcc Ser 250	agt Ser	ata Ile	ctt Leu	tca Ser	cta Leu 255	gag Glu	ata Ile	cgg Arg	gac Asp	gtt Val 260	ctg Leu	gaa Glu	821
tat Tyr	ggt Gly	tgg Trp 265	cac His	acc Thr	aat Asn	ttg Leu	cca Pro 270	cgc Arg	ttg Leu	gaa Glu	gca Ala	agg Arg 275	aat Asn	tac Tyr	atg Met	869
gac Asp	gtc Val 280	ttt Phe	gga Gly	cag Gln	cac His	act Thr 285	aaa Lys	aat Asn	aag Lys	aac Asn	gcc Ala 290	gcc Ala	gag Glu	aaa Lys	ctt Leu	917
tta Leu 295	gaa Glu	ctt Leu	gca Ala	aaa Lys	ttg Leu 300	gaa Glu	ttc Phe	aat Asn	ata Ile	ttt Phe 305	cac His	tcc Ser	tta Leu	caa Gln	gag Glu 310	965
aga Arg	gag Glu	tta Leu	aaa Lys	cat His 315	gtt Val	tcc Ser	cga Arg	tgg Trp	tgg Trp 320	aaa Lys	gac Asp	tcg Ser	ggt Gly	tct Ser 325	cct Pro	1013
gag Glu	atg Met	acc Thr	ttc Phe 330	tgt Cys	cga Arg	cat His	cgt Arg	cac His 335	gtg Val	gaa Glu	tac Tyr	tac Tyr	gct Ala 340	ttg Leu	gct Ala	1061
tcc Ser	tgc Cys	att Ile 345	gcg Ala	ttc Phe	gag Glu	cct Pro	caa Gln 350	cat His	tct Ser	gga Gly	ttc Phe 355	aga Arg	ctc Leu	ggc Gly	ttt Phe	1109
acc Thr	aag Lys 360	atg Met	tct Ser	cat His	ctt Leu	atc Ile 365	acg Thr	gtt Val	ctt Leu	gac Asp	gac Asp 370	atg Met	tac Tyr	gac Asp	gtc Val	1157
ttc Phe 375	ggc Gly	aca Thr	gta Val	gac Asp	gag Glu 380	ctg Leu	gaa Glu	ctc Leu	ttc Phe	aca Thr 385	gcg Ala	aca Thr	att Ile	aag Lys	aga Arg 390	1205
tgg Trp	gat Asp	ccg Pro	tcc Ser	gcg Ala 395	atg Met	gaa Glu	tgc Cys	ctt Leu	cca Pro 400	gaa Glu	tat Tyr	atg Met	aaa Lys	gga Gly 405	gtg Val	1253
tac	atg	atg	gtt	tat	cac	acc	gta	aat	gaa	atg	gct	cga	gtg	gca	gag	1301

Tyr Met Met Val Tyr His Thr Val Asn Glu Met Ala Arg Val Ala Glu
410 415 420

aag gct caa ggc cga gac acg ctc aac tat gca aga cag gct tgg gag 1349
Lys Ala Gln Gly Arg Asp Thr Leu Asn Tyr Ala Arg Gln Ala Trp Glu
425 430 435

gcg tgt ttt gat tcg tat atg cag gaa gca aag tgg atc gcc act ggt 1397
Ala Cys Phe Asp Ser Tyr Met Gln Glu Ala Lys Trp Ile Ala Thr Gly
440 445 450

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Tyr Leu Pro Thr Phe Glu Glu Tyr Leu Glu Asn Gly Lys Val Ser Ser
455 460 465 470

gct cat cgc cca tgc gca ctg caa ccc att ctg acg ttg gac atc ccc 1493
Ala His Arg Pro Cys Ala Leu Gln Pro Ile Leu Thr Leu Asp Ile Pro
475 480 485

ttt cct gat cac atc ctc aag gaa gtt gac ttc cca tcg aag ctc aat 1541
Phe Pro Asp His Ile Leu Lys Glu Val Asp Phe Pro Ser Lys Leu Asn
490 495 500

gac ttg ata tgt atc atc ctt cga tta aga ggt gat aca cgg tgc tac 1589
Asp Leu Ile Cys Ile Ile Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr
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Met Lys Asp Asn Pro Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile
535 540 545 550

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Asn Phe Met Ile Arg Asp Ala Ile Arg Glu Leu Asn Trp Glu Leu Leu
555 560 565

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Lys Pro Asp Asn Ser Val Pro Ile Thr Ser Lys Lys His Ala Phe Asp
570 575 580

ata agc aga gtt tgg cat cac ggt tac aga tac cga gat ggc tac agc 1829
Ile Ser Arg Val Trp His His Gly Tyr Arg Tyr Arg Asp Gly Tyr Ser
585 590 595

ttt gcc aac gtt gaa aca aag agt ttg gtg atg aga acc gtc att gaa 1877
Phe Ala Asn Val Glu Thr Lys Ser Leu Val Met Arg Thr Val Ile Glu
600 605 610

cct gtg cct ttg taacaacact tcaaactctac aatattaact gaggatgccc 1929
Pro Val Pro Leu
615

tatgggtgta tatagggcac acaaaaataa atatggttgt gttagtaaag ctgtaattta 1989

tgaaaaaaaa aaaaaaaaaa aaaa 2013

<211> 618

<212> PRT

<213> Abies grandis

<400> 65

Met Ala Leu Leu Ser Ile Thr Pro Leu Val Ser Arg Ser Cys Leu Ser
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Ser Ser His Glu Ile Lys Ala Leu Arg Arg Thr Ile Pro Thr Leu Gly
20 25 30

Ile Cys Arg Pro Gly Lys Ser Val Ala His Ser Ile Asn Met Cys Leu
35 40 45

Thr Ser Val Ala Ser Thr Asp Ser Val Gln Arg Arg Val Gly Asn Tyr
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Val Val Thr Asp Leu Asn Ser Thr Ala Leu Gly Leu Arg Thr Leu Arg
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Gly Glu Lys Val Met Asp Glu Ala Glu Thr Phe Ser Thr Lys Tyr Leu
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Ile Arg Asp Val Leu Glu Tyr Gly Trp His Thr Asn Leu Pro Arg Leu
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Glu Ala Arg Asn Tyr Met Asp Val Phe Gly Gln His Thr Lys Asn Lys
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Asn Ala Ala Glu Lys Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile
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Tyr	Ser	Tyr	Trp	Asn	Glu	Lys	Gly	Ile	Gly	Cys	Gly	Arg	Asp	Ser	Val	
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acc gtt ctg aat tta tat cgg gct tct ttc att gcc ttt cct ggg gag Thr Val Leu Asn Leu Tyr Arg Ala Ser Phe Ile Ala Phe Pro Gly Glu 220 225 230			726
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Tyr Thr Gln Glu Ala Lys Trp Ile Ala Ser Gly Tyr Leu Pro Thr Phe	
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Glu Glu Tyr Leu Glu Asn Ala Lys Val Ser Ser Gly His Arg Ala Ala	
475 480 485	
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Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys Ala Asp Arg Asp	
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Gly Leu Thr Glu Glu Asp Ala Leu Asn His Ile Asn Ala Met Ile Asn	
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Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Lys Pro Asp Ser Asn	
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Ile Pro Met Thr Ala Arg Lys His Ala Tyr Glu Ile Thr Arg Ala Phe	
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His Gln Leu Tyr Lys Tyr Arg Asp Gly Phe Ser Val Ala Thr Gln Glu	
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Asp Ser Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys Lys Glu Ile
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Gly Cys Gly Arg Asp Ser Val Phe Pro Asp Val Asn Ser Thr Ala Ser
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Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Ser Val Ser Ser Glu Val
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Leu Lys Val Phe Gln Asp Gln Asn Gly Gln Phe Ala Phe Ser Pro Ser
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Thr Lys Glu Arg Asp Ile Arg Thr Val Leu Asn Leu Tyr Arg Ala Ser
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Gln Gln Lys Glu Leu Gln Tyr Ile Ser Arg Trp Trp Lys Asp Ser Cys	
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Ser Ser His Leu Thr Phe Thr Arg His Arg His Val Glu Tyr Tyr Thr	
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Val Pro Leu Pro Asn Tyr Ile Leu Gln Glu Ile Asp Tyr Pro Ser Arg
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Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Ala Ile Ser
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His Ile Asn Val Met Ile Ser Asp Ala Ile Arg Glu Leu Asn Trp Glu
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 Val Ile Asn Met Lys Leu Thr Thr Val Ser His Arg Asp Asp Asn Gly
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 Tyr Ser Glu Arg Ala Val Thr Val Val Glu Glu Val Lys Glu Met Phe
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 Asn Ser Ile Pro Asn Asn Arg Glu Leu Phe Gly Ser Gln Asn Asp Leu
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 Leu Thr Arg Leu Trp Met Val Asp Ser Ile Glu Arg Leu Gly Ile Asp
 130 135 140
 Arg His Phe Gln Asn Glu Ile Arg Val Ala Leu Asp Tyr Val Tyr Ser
 145 150 155 160
 Tyr Trp Lys Glu Lys Glu Gly Ile Gly Cys Gly Arg Asp Ser Thr Phe
 165 170 175
 Pro Asp Leu Asn Ser Thr Ala Leu Ala Leu Arg Thr Leu Arg Leu His
 180 185 190
 Gly Tyr Asn Val Ser Ser Asp Val Leu Glu Tyr Phe Lys Asp Gln Lys
 195 200 205
 Gly His Phe Ala Cys Pro Ala Ile Leu Thr Glu Gly Gln Ile Thr Arg
 210 215 220
 Ser Val Leu Asn Leu Tyr Arg Ala Ser Leu Val Ala Phe Pro Gly Glu

225		230		235		240
Lys Val Met Glu	Glu Ala Glu Ile Phe Ser	Ala Ser Tyr Leu	Lys Glu			
	245		250		255	
Val Leu Gln Lys	Ile Pro Val Ser Ser	Phe Ser Arg Glu	Ile Glu Tyr			
	260	265	270			
Val Leu Glu Tyr	Gly Trp His Thr	Asn Leu Pro Arg	Leu Glu Ala Arg			
	275	280	285			
Asn Tyr Ile Asp	Val Tyr Gly Gln Asp	Ser Tyr Glu Ser	Ser Asn Glu			
	290	295	300			
Met Pro Tyr Val	Asn Thr Gln Lys Leu	Leu Lys Leu Ala	Lys Leu Glu			
	305	310	315		320	
Phe Asn Ile Phe	His Ser Leu Gln Gln	Lys Glu Leu Gln	Tyr Ile Ser			
	325	330	335			
Arg Trp Trp Lys	Asp Ser Cys Ser	Ser His Leu Thr	Phe Thr Arg His			
	340	345	350			
Arg His Val Glu	Tyr Tyr Thr Met	Ala Ser Cys Ile	Ser Met Glu Pro			
	355	360	365			
Lys His Ser Ala	Phe Arg Leu Gly	Phe Val Lys Thr	Cys His Leu Leu			
	370	375	380			
Thr Val Leu Asp	Asp Met Tyr Asp	Thr Phe Gly Thr	Leu Asp Glu Leu			
	385	390	395		400	
Gln Leu Phe Thr	Thr Ala Phe Lys	Arg Trp Asp Leu	Ser Glu Thr Lys			
	405	410	415			
Cys Leu Pro Glu	Tyr Met Lys Ala	Val Tyr Met Asp	Leu Tyr Gln Cys			
	420	425	430			
Leu Asn Glu Leu	Ala Gln Glu Ala	Glu Lys Thr Gln	Gly Arg Asp Thr			
	435	440	445			
Leu Asn Tyr Ile	Arg Asn Ala Tyr	Glu Ser His Phe	Asp Ser Phe Met			
	450	455	460			
His Glu Ala Lys	Trp Ile Ser Ser	Gly Tyr Leu Pro	Thr Phe Glu Glu			
	465	470	475		480	
Tyr Leu Lys Asn	Gly Lys Val Ser	Ser Gly Ser Arg	Thr Ala Thr Leu			
	485	490	495			
Gln Pro Ile Leu	Thr Leu Asp Val	Pro Leu Pro Asn	Tyr Ile Leu Gln			
	500	505	510			
Glu Ile Asp Tyr	Pro Ser Arg Phe	Asn Asp Leu Ala	Ser Ser Leu Leu			
	515	520	525			
Arg Leu Arg Gly	Asp Thr Arg Cys	Tyr Lys Ala Asp	Arg Ala Arg Gly			
	530	535	540			
Glu Glu Ala Ser	Ala Ile Ser Cys	Tyr Met Lys Asp	His Pro Gly Ser			
	545	550	555	560		

Thr Glu Glu Asp Ala Leu Asn His Ile Asn Val Met Ile Ser Asp Ala
565 570 575

Ile Arg Glu Leu Asn Trp Glu Leu Leu Arg Pro Asp Ser Lys Ser Pro
580 585 590

Ile Ser Ser Lys Lys His Ala Phe Asp Ile Thr Arg Ala Phe His His
595 600 605

Leu Tyr Lys Tyr Arg Asp Gly Tyr Thr Val Ala Ser Ser Glu Thr Lys
610 615 620

Asn Leu Val Met Lys Thr Val Leu Glu Pro Val Ala Leu
625 630 635

<210> 70
<211> 696
<212> DNA
<213> *Abies grandis*

<400> 70
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cgagagacgc tcaacgatgc tcgacgagct tgggaggcct atcttgattc gtatatgaaa 180
gaagctgagt ggatctccag tgggttatctg ccaacgtttg aggagtacat ggagaccagc 240
aaagttagtt ttggttatcg catattcgca ttgcaacca tcctcactat ggatgttccc 300
cttactcacc acatcctgca ggaaatagac tttccattga ggtttaatga cttaatatgt 360
tccatccttc gacttaaaaa tgacactcgc tgctacaagg cggacagggc ccgtggagaa 420
gaagcttcgt gtatatcgtg ttatatgaaa gagaatcctg gatcaacaga ggaagatgct 480
atcaatcata tcaacgctat ggtcaataac ttaatcaaag aagtgaattg ggagcttctc 540
cgacaggacg gcaccgctca tattgcttgc aagaaacacg cttttgacat cctcaaaggt 600
tcccttcacg gctacaaata ccgagatggg ttcagcgttg ccaacaagga aaccaagaat 660
tgggtgagga gaacagtcct tgagtctgtg cctttg 696

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<220>
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<222> (1)..(20)
<223> Reverse RACE primer 10-2

<400> 71
acgaagcttc ttctccacgg

20

<210> 72
<211> 20
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<213> Artificial Sequence

<220>
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oligonucleotide

<220>
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<222> (1)..(20)
<223> Reverse RACE primer 10-4

<400> 72
ggatcccatc tcttaactgc

20

<210> 73
<211> 27
<212> DNA
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oligonucleotide

<220>
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<222> (1)..(27)
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<400> 73
ccatcctaatac gactcact atagggc

27

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oligonucleotide

<220>
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<222> (1)..(23)
<223> PCR primer AP2

<400> 74
actcactata gggctcgagc ggc

23

<210> 75
<211> 24

<212> DNA
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<220>

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<223> PCR primer AG9F

<400> 75

atggctcttg tttctatctt gccc

24

<210> 76

<211> 24

<212> DNA

<213> Artificial Sequence

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<222> (1)..(24)

<223> PCR primer AG9R

<400> 76

ttacaaaggc acagactcaa ggac

24

<210> 77

<211> 1890

<212> DNA

<213> Abies grandis

<220>

<221> CDS

<222> (1)..(1890)

<400> 77

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Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
1 5 10 15

aaa tcg tgg atc gtt tct act tat gag cat aag gct atc agt aga aca 96
Lys Ser Trp Ile Val Ser Thr Tyr Glu His Lys Ala Ile Ser Arg Thr
20 25 30

atc cca aat ctt gga ttg cgt ggg cga ggg aaa tct gtg aca cat tcc 144
Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
35 40 45

ctg aga atg agt ttg agc acc gca gtc tct gat gat cat ggt gta caa 192
Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
50 55 60

aga cgc ata gtc gag ttt cat tcc aat ctg tgg gac gac gat ttc ata 240

Arg 65	Arg	Ile	Val	Glu	Phe 70	His	Ser	Asn	Leu	Trp 75	Asp	Asp	Asp	Phe	Ile 80	
caa	tct	cta	tca	acg	cct	tat	ggg	gca	cct	tca	tac	cgt	gaa	cgt	gct	288
Gln	Ser	Leu	Ser	Thr 85	Pro	Tyr	Gly	Ala	Pro 90	Ser	Tyr	Arg	Glu	Arg 95	Ala	
gat	aga	ctt	att	gtg	gaa	gta	aag	ggg	ata	ttc	act	tca	att	tca	gcg	336
Asp	Arg	Leu	Ile 100	Val	Glu	Val	Lys	Gly 105	Ile	Phe	Thr	Ser	Ile 110	Ser	Ala	
gaa	gat	gga	gaa	cta	atc	act	ccc	ctc	aat	gat	ctc	att	caa	cgc	ctt	384
Glu	Asp	Gly 115	Glu	Leu	Ile	Thr	Pro 120	Leu	Asn	Asp	Leu	Ile 125	Gln	Arg	Leu	
tta	atg	gtc	gat	aac	gtt	gaa	cgt	tta	ggg	att	gat	aga	cat	ttc	aaa	432
Leu	Met 130	Val	Asp	Asn	Val	Glu	Arg 135	Leu	Gly	Ile 140	Asp	Arg	His	Phe	Lys	
aat	gag	ata	aaa	gca	gca	cta	gac	tat	gtt	tac	agt	tat	tgg	aac	gaa	480
Asn	Glu	Ile	Lys	Ala	Ala 150	Leu	Asp	Tyr	Val 155	Tyr	Ser	Tyr	Trp	Asn	Glu 160	
aaa	ggc	att	ggc	agt	gga	agt	gat	agt	ggg	gtt	gct	gat	ctc	aac	tca	528
Lys	Gly	Ile	Gly 165	Ser	Gly	Ser	Asp	Ser 170	Gly	Val	Ala	Asp	Leu	Asn 175	Ser	
act	gcc	ctg	ggg	ttt	cga	att	ctt	cga	cta	cac	gga	tac	agt	gtt	tct	576
Thr	Ala	Leu	Gly 180	Phe	Arg	Ile	Leu	Arg 185	Leu	His	Gly	Tyr	Ser 190	Val	Ser	
tca	gat	gtg	ttg	gaa	cac	ttc	aaa	gag	gag	aag	gag	aag	ggg	cag	ttt	624
Ser	Asp	Val 195	Leu	Glu	His	Phe	Lys 200	Glu	Glu	Lys	Glu	Lys 205	Gly	Gln	Phe	
gta	tgt	tcg	gcc	atc	caa	aca	gag	gaa	gag	ata	aaa	agc	gtt	ctg	aat	672
Val	Cys 210	Ser	Ala	Ile	Gln	Thr 215	Glu	Glu	Glu	Ile	Lys 220	Ser	Val	Leu	Asn	
tta	ttt	cgg	gcc	tcc	ctc	att	gcc	ttt	cct	ggg	gag	aaa	gtt	atg	gaa	720
Leu	Phe 225	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly 235	Glu	Lys	Val	Met	Glu 240	
gag	gct	gaa	atc	ttc	tct	aaa	ata	tat	tta	aaa	gaa	gcc	tta	caa	aat	768
Glu	Ala	Glu	Ile 245	Phe	Ser	Lys	Ile	Tyr 250	Leu	Lys	Glu	Ala	Leu	Gln 255	Asn	
att	gct	gtc	tcc	agt	ctt	tca	cga	gag	ata	gag	tac	gtt	ctg	gag	gat	816
Ile	Ala	Val	Ser 260	Ser	Leu	Ser	Arg	Glu 265	Ile	Glu	Tyr	Val	Leu 270	Glu	Asp	
ggg	tgg	caa	aca	aat	atg	cca	aga	ttg	gaa	aca	agg	aac	tac	atc	gat	864
Gly	Trp	Gln 275	Thr	Asn	Met	Pro	Arg 280	Leu	Glu	Thr	Arg	Asn 285	Tyr	Ile	Asp	
gta	ttg	gga	gag	aac	gat	cgt	gat	gag	acg	tta	tat	atg	aac	atg	gag	912
Val	Leu 290	Gly	Glu	Asn	Asp	Arg 295	Asp	Glu	Thr	Leu	Tyr 300	Met	Asn	Met	Glu	
aaa	ctt	tta	gaa	att	gca	aaa	ttg	gag	ttc	aat	att	ttt	cac	tcc	tta	960
Lys	Leu	Leu	Glu	Ile	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu	

305	310	315	320	
caa cag aga gag cta aaa gac ctc tcc aga tgg tgg aaa gat tcg ggt				1008
Gln Gln Arg Glu Leu Lys Asp Leu Ser Arg Trp Trp Lys Asp Ser Gly	325	330	335	
ttc tct cac ctg aca ttt tct cgg cat cgt cat gtg gaa ttc tac gct				1056
Phe Ser His Leu Thr Phe Ser Arg His Arg His Val Glu Phe Tyr Ala	340	345	350	
ctg gca tct tgc att gaa act gat cgc aaa cat tcc gga ttc aga ctc				1104
Leu Ala Ser Cys Ile Glu Thr Asp Arg Lys His Ser Gly Phe Arg Leu	355	360	365	
ggc ttt gcc aaa atg tgt cat ctt atc acg gtt ttg gac gat ata tac				1152
Gly Phe Ala Lys Met Cys His Leu Ile Thr Val Leu Asp Asp Ile Tyr	370	375	380	
gac acc ttt gga aca atg gag gag ctg gaa ctc ttc act gca gca ttt				1200
Asp Thr Phe Gly Thr Met Glu Glu Leu Glu Leu Phe Thr Ala Ala Phe	385	390	395	400
aag aga tgg gat ccg tct gcc aca gat ttg ctt cca gag tat atg aaa				1248
Lys Arg Trp Asp Pro Ser Ala Thr Asp Leu Leu Pro Glu Tyr Met Lys	405	410	415	
ggg ttg tac atg gtg gtt tac gaa acc gta aat gaa att gct cga gag				1296
Gly Leu Tyr Met Val Val Tyr Glu Thr Val Asn Glu Ile Ala Arg Glu	420	425	430	
gca gac aag tct caa ggc cga gag acg ctc aac gat gct cga cga gct				1344
Ala Asp Lys Ser Gln Gly Arg Glu Thr Leu Asn Asp Ala Arg Arg Ala	435	440	445	
tgg gag gcc tat ctt gat tcg tat atg aaa gaa gct gag tgg atc tcc				1392
Trp Glu Ala Tyr Leu Asp Ser Tyr Met Lys Glu Ala Glu Trp Ile Ser	450	455	460	
agt ggt tat ctg cca acg ttt gag gag tac atg gag acc agc aaa gtt				1440
Ser Gly Tyr Leu Pro Thr Phe Glu Glu Tyr Met Glu Thr Ser Lys Val	465	470	475	480
agt ttt ggt tat cgc ata ttc gca ttg caa ccc atc ctc act atg gat				1488
Ser Phe Gly Tyr Arg Ile Phe Ala Leu Gln Pro Ile Leu Thr Met Asp	485	490	495	
gtt ccc ctt act cac cac atc ctg cag gaa ata gac ttt cca ttg agg				1536
Val Pro Leu Thr His His Ile Leu Gln Glu Ile Asp Phe Pro Leu Arg	500	505	510	
ttt aat gac tta ata tgt tcc atc ctt cga ctt aaa aat gac act cgc				1584
Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg	515	520	525	
tgc tac aag gcg gac agg gcc cgt gga gaa gaa gct tcg tgt ata tcg				1632
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser	530	535	540	
tgt tat atg aaa gag aat cct gga tca aca gag gaa gat gct atc aat				1680
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn	545	550	555	560

1008 1056 1104 1152 1200 1248 1296 1344 1392 1440 1488 1536 1584 1632 1680

cat atc aac gct atg gtc aat aac tta atc aaa gaa gtg aat tgg gag	1728
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu	
565 570 575	
ctt ctc cga cag gac ggc acc gct cat att gct tgc aag aaa cac gct	1776
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala	
580 585 590	
ttt gac atc ctc aaa ggt tcc ctt cac ggc tac aaa tac cga gat ggg	1824
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly	
595 600 605	
ttc agc gtt gcc aac aag gaa acc aag aat tgg gtg agg aga aca gtc	1872
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val	
610 615 620	
ctt gag tct gtg cct ttg	1890
Leu Glu Ser Val Pro Leu	
625 630	

<210> 78
 <211> 630
 <212> PRT
 <213> Abies grandis

<400> 78
 Met Ala Leu Val Ser Ile Leu Pro Leu Ser Ser Lys Ser Val Leu His
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 20 25 30
 Ile Pro Asn Leu Gly Leu Arg Gly Arg Gly Lys Ser Val Thr His Ser
 35 40 45
 Leu Arg Met Ser Leu Ser Thr Ala Val Ser Asp Asp His Gly Val Gln
 50 55 60
 Arg Arg Ile Val Glu Phe His Ser Asn Leu Trp Asp Asp Asp Phe Ile
 65 70 75 80
 Gln Ser Leu Ser Thr Pro Tyr Gly Ala Pro Ser Tyr Arg Glu Arg Ala
 85 90 95
 Asp Arg Leu Ile Val Glu Val Lys Gly Ile Phe Thr Ser Ile Ser Ala
 100 105 110
 Glu Asp Gly Glu Leu Ile Thr Pro Leu Asn Asp Leu Ile Gln Arg Leu
 115 120 125
 Leu Met Val Asp Asn Val Glu Arg Leu Gly Ile Asp Arg His Phe Lys
 130 135 140
 Asn Glu Ile Lys Ala Ala Leu Asp Tyr Val Tyr Ser Tyr Trp Asn Glu
 145 150 155 160
 Lys Gly Ile Gly Ser Gly Ser Asp Ser Gly Val Ala Asp Leu Asn Ser
 165 170 175

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Thr	Ala	Leu	Gly	Phe	Arg	Ile	Leu	Arg	Leu	His	Gly	Tyr	Ser	Val	Ser	
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Ser	Asp	Val	Leu	Glu	His	Phe	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Gln	Phe	
		195					200					205				
Val	Cys	Ser	Ala	Ile	Gln	Thr	Glu	Glu	Glu	Ile	Lys	Ser	Val	Leu	Asn	
	210					215					220					
Leu	Phe	Arg	Ala	Ser	Leu	Ile	Ala	Phe	Pro	Gly	Glu	Lys	Val	Met	Glu	
225					230					235					240	
Glu	Ala	Glu	Ile	Phe	Ser	Lys	Ile	Tyr	Leu	Lys	Glu	Ala	Leu	Gln	Asn	
				245					250					255		
Ile	Ala	Val	Ser	Ser	Leu	Ser	Arg	Glu	Ile	Glu	Tyr	Val	Leu	Glu	Asp	
			260					265					270			
Gly	Trp	Gln	Thr	Asn	Met	Pro	Arg	Leu	Glu	Thr	Arg	Asn	Tyr	Ile	Asp	
		275					280					285				
Val	Leu	Gly	Glu	Asn	Asp	Arg	Asp	Glu	Thr	Leu	Tyr	Met	Asn	Met	Glu	
	290					295					300					
Lys	Leu	Leu	Glu	Ile	Ala	Lys	Leu	Glu	Phe	Asn	Ile	Phe	His	Ser	Leu	
305					310					315					320	
Gln	Gln	Arg	Glu	Leu	Lys	Asp	Leu	Ser	Arg	Trp	Trp	Lys	Asp	Ser	Gly	
				325					330					335		
Phe	Ser	His	Leu	Thr	Phe	Ser	Arg	His	Arg	His	Val	Glu	Phe	Tyr	Ala	
			340					345					350			
Leu	Ala	Ser	Cys	Ile	Glu	Thr	Asp	Arg	Lys	His	Ser	Gly	Phe	Arg	Leu	
		355					360					365				
Gly	Phe	Ala	Lys	Met	Cys	His	Leu	Ile	Thr	Val	Leu	Asp	Asp	Ile	Tyr	
	370					375					380					
Asp	Thr	Phe	Gly	Thr	Met	Glu	Glu	Leu	Glu	Leu	Phe	Thr	Ala	Ala	Phe	
385					390					395					400	
Lys	Arg	Trp	Asp	Pro	Ser	Ala	Thr	Asp	Leu	Leu	Pro	Glu	Tyr	Met	Lys	
				405					410					415		
Gly	Leu	Tyr	Met	Val	Val	Tyr	Glu	Thr	Val	Asn	Glu	Ile	Ala	Arg	Glu	
			420					425					430			
Ala	Asp	Lys	Ser	Gln	Gly	Arg	Glu	Thr	Leu	Asn	Asp	Ala	Arg	Arg	Ala	
		435					440					445				
Trp	Glu	Ala	Tyr	Leu	Asp	Ser	Tyr	Met	Lys	Glu	Ala	Glu	Trp	Ile	Ser	
	450					455					460					
Ser	Gly	Tyr	Leu	Pro	Thr	Phe	Glu	Glu	Tyr	Met	Glu	Thr	Ser	Lys	Val	
465					470					475					480	
Ser	Phe	Gly	Tyr	Arg	Ile	Phe	Ala	Leu	Gln	Pro	Ile	Leu	Thr	Met	Asp	
				485					490					495		
Val	Pro	Leu	Thr	His	His	Ile	Leu	Gln	Glu	Ile	Asp	Phe	Pro	Leu	Arg	

500	505	510
Phe Asn Asp Leu Ile Cys Ser Ile Leu Arg Leu Lys Asn Asp Thr Arg 515	520	525
Cys Tyr Lys Ala Asp Arg Ala Arg Gly Glu Glu Ala Ser Cys Ile Ser 530	535	540
Cys Tyr Met Lys Glu Asn Pro Gly Ser Thr Glu Glu Asp Ala Ile Asn 545	550	555
His Ile Asn Ala Met Val Asn Asn Leu Ile Lys Glu Val Asn Trp Glu 565	570	575
Leu Leu Arg Gln Asp Gly Thr Ala His Ile Ala Cys Lys Lys His Ala 580	585	590
Phe Asp Ile Leu Lys Gly Ser Leu His Gly Tyr Lys Tyr Arg Asp Gly 595	600	605
Phe Ser Val Ala Asn Lys Glu Thr Lys Asn Trp Val Arg Arg Thr Val 610	615	620
Leu Glu Ser Val Pro Leu 625	630	

<210> 79
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<220>
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 <223> Mutagenesis primer 6eBamHIF

<400> 79
 caattaagag atgggacccg tccgcgatgg

30

<210> 80
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 <212> DNA
 <213> Artificial Sequence

<220>
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 <223> Mutagenesis primer 6eBamHIR

<400> 80
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30

<210> 81
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<212> DNA
<213> Artificial Sequence

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oligonucleotide

<220>
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<223> Mutagenesis primer 9eBamHIF

<400> 81
gcatttaaga gatgggaccc gtctgccaca

30

<210> 82
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<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<220>
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<223> Mutagenesis primer 9eBamHIR

<400> 82
ctgtggcaga cgggtcccat ctcttaaag

30

<210> 83
<211> 25
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(25)
<223> Mutagenesis primer 732eNdeIF

<400> 83
cgagatgccca tacgtgaata cgcag

25

<210> 84
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(25)
<223> mutagenesis primer 732eNde1R

<400> 84
ctgcgtattc acgtatggca tctcg

25

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(30)
<223> PCR primer 6-Nde1-M

<400> 85
ctgatagcaa gctcatatgg ctcttctttc

30

<210> 86
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
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<222> (1)..(34)
<223> PCR primer 6-NdeI-R

<400> 86
gcccacgcgt ctcatatgag aatcagtaga tgcg

34

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<220>
<221> misc_feature
<222> (1)..(29)

29

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<220>  
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